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USSN 10/663,450  
Page 2**AMENDMENTS TO THE CLAIMS:**

The following Listing of Claims will replace all prior listings, and version of claims in the application.

1. (Cancelled)
2. (Currently Amended): A method of increasing the secretion of a heterologous protein in a eukaryotic fungal cell, comprising  
inducing an unfolded protein response (UPR) by increasing the presence of a HAC1 UPR-modulating protein in said eukaryotic fungal cell, comprising transforming the eukaryotic fungal cell with a nucleic acid encoding the a fungal HAC1 UPR-modulating protein comprising a DNA binding domain having at least 90% sequence identity to a DNA binding domain of:
  - a) amino acid residues 84 – 147 of SEQ ID NO: 5;
  - b) amino acid residues 53 – 116 of SEQ ID NO: 6 or
  - c) amino acid residues 45 – 109 of SEQ ID No:19, andincreasing secretion of the heterologous protein relative to secretion of the heterologous protein in a parental cell.
3. (Original): The method of Claim 2 wherein said HAC1 protein is constitutively produced.
4. (Cancelled)
5. (Original): The method of Claim 2 wherein said HAC1 protein is encoded by a nucleic acid isolated from a cell selected from the group consisting of *Aspergillus*, *Trichoderma*, *Saccharomyces*, *Schizosaccharomyces*, *Kluyveromyces*, *Pichia*, *Hansenula*, *Fusarium*, *Neurospora*, and *Penicillium*.
6. (Original): The method of Claim 2 wherein said HAC1 protein is encoded by a nucleic acid isolated from yeast.
7. (Original): The method of Claim 6 wherein said yeast is *Saccharomyces cerevisiae*.

GC590-2-C1 ROA 8.15.07

USSN 10/663,450  
Page 3

8. (Original): The method of Claim 2 wherein said HAC1 protein is encoded by a nucleic acid isolated from filamentous fungi.
9. (Original): The method of Claim 8 wherein said fungi is from *Trichoderma*.
10. (Original): The method of Claim 8 wherein said fungi is *Trichoderma reesei*.
11. (Original): The method of Claim 8 wherein said fungi is from *Aspergillus*.
12. (Original): The method of Claim 8 wherein said fungi is *Aspergillus nidulans*.
13. (Original): The method of Claim 8 wherein said fungi is *Aspergillus niger*.
- 14- 25. (Cancelled)
26. (Currently amended): The method of Claim 2 wherein said eukaryotic fungal cell is selected from the group consisting of *Aspergillus spp.*, *Trichoderma spp.*, *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces spp.*, *Pichia spp.*, *Hansenula polymorpha*, *Fusarium spp.*, *Neurospora spp.*, and *Penicillium spp.*
27. (Currently amended): The method of Claim 2 wherein said eukaryotic fungal cell is a yeast cell.
28. (Original): The method of Claim 27 wherein said yeast is *Saccharomyces cerevisiae*.
29. (Currently amended): The method of Claim 2 wherein said eukaryotic fungal cell is a filamentous fungi.
30. (Original): The method of Claim 29 wherein said fungi is from *Trichoderma*.
31. (Original): The method of Claim 29 wherein said fungi is *Trichoderma reesei*.
32. (Original): The method of Claim 29 wherein said fungi is from *Aspergillus*.
33. (Original): The method of Claim 29 wherein said fungi is *Aspergillus nidulans*.
34. (Original): The method of Claim 29 wherein said fungi is *Aspergillus niger*.

GC590-2-C1 ROA 8.15.07

USSN 10/663,450

Page 4

**35-82. (Cancelled)**

83. (Withdrawn and amended) A fungal cell containing a heterologous nucleic acid encoding a yeast or filamentous fungi protein having unfolded protein response modulating activity and a heterologous nucleic acid encoding a protein of interest to be secreted.

84. (Withdrawn): The cell of Claim 83 wherein said protein having unfolded protein response modulating activity is a fungal HAC1.

85. (Withdrawn): The cell of Claim 83 wherein said protein of interest is selected from the group consisting of lipase, cellulase, endo-glucosidase H, protease, carbohydrase, reductase, oxidase, isomerase, transferase, kinase, phosphatase, alpha-amylase, glucoamylase, lignocellulose hemicellulase, pectinase and ligninase.

**86. (Cancelled)**

87. (Withdrawn): The cell of Claim 83 wherein said protein having unfolded protein response modulating activity is a yeast HAC1.

**88. (Cancelled):**

89. (Previously presented): The method of Claim 2 wherein said UPR-modulating protein comprises a DNA binding domain that has at least 90% identity to the DNA binding domain of a) amino acid residues 84 – 147 of SEQ ID NO: 5 or b) amino acid residues 53 – 116 of SEQ ID NO: 6.

90. (Currently amended): The method of Claim 2 wherein said UPR-modulating protein comprises a DNA binding domain that has at least 95% identity to the DNA binding domain of a) amino acid residues 84 – 147 of SEQ ID No: 5 or b) amino acid residues 53 – 116 of SEQ ID No: 6 or c) amino acid residues 45 – ~~[[116]]~~109 of SEQ ID No: 19.

91. (Previously presented): The method of Claim 2 wherein said UPR-modulating protein comprises a DNA binding domain having the DNA binding domain of amino acid residue positions 84 to 147 of SEQ ID NO: 5.

USSN 10/663,450

Page 5

92. (Previously presented): The method of Claim 2 wherein said UPR-modulating protein comprises a DNA binding domain having the DNA binding domain of amino acid residue positions of 53 to 116 of SEQ ID NO: 6.
93. (Previously presented): The method of Claim 2, wherein said heterologous protein is selected from the group consisting of lipases, cellulases, endo-glucosidase H, proteases, carbohydrases, reductases, oxidases, isomerases, transferases, kinases, phosphatases, alpha-amylases, glucoamylases, hemicellulases, pectinases and ligninases.
94. (Previously presented): The method of Claim 93, wherein the heterologous protein is a protease, cellulase, glucoamylase or alpha amylase.
95. (Currently amended): The method of Claim 2, wherein the ~~eukaryotic~~ fungal cell is a *Trichoderma* or *Aspergillus* fungal cell, the UPR-modulating protein comprising a DNA binding domain has at least 90% sequence identity to the DNA binding domain of a) amino acid residues 84 – 147 of SEQ ID NO: 5 or b) amino acid residues 53 – 116 of SEQ ID NO: 6 and the heterologous protein is selected from the group consisting of proteases, cellulases, glucoamylases, and alpha amylases ~~and combination thereof~~.
96. (Currently amended): The method of Claim 95, wherein the ~~eukaryotic~~ fungal cell is a *Trichoderma* cell and the UPR-modulating protein comprises a DNA binding domain that has at least 95% sequence identity to the DNA binding domain of a) amino acid residues 84 – 147 of SEQ ID NO: 5 or b) amino acid residues 53 – 116 of SEQ ID NO: 6.
97. (Currently amended): The method of Claim 95, wherein the ~~eukaryotic~~ fungal cell is an *Aspergillus* cell and the UPR-modulating protein comprises a DNA binding domain that has at least 95% sequence similarity to the DNA binding domain of a) amino acid residues 84 – 147 of SEQ ID NO: 5; b) amino acid residues 53 – 116 of SEQ ID NO: 6.
98. (Previously presented): The method of Claim 2, further comprising a promoter operably linked to the nucleic acid encoding the HAC1 UPR-modulating protein, said promoter selected from the group consisting of *cbh1*, *gpdA*, *adh1* and *pgk1*.

GC590-2-C1 ROA 8.15.07